EVOLUZIONE 2017

7° Congresso della Società Italiana di Biologia Evoluzionistica

Abstracts book

Rome, 28-31 August 2017

Department of Sciences, Roma Tre University, viale G.Marconi 446

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Multiple sources of incongruence in *Wolbachia* phylogeny

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Wolbachia are maternally inherited intracellular endosymbionts bacteria, commonly found in the reproductive tissues of arthropods and nematodes. Because of its ability to manipulate host's reproduction and influence the transmissibility of host's pathogens, *Wolbachia* has substantial implications on the host species evolution and is a promising biological tool to control diseases and invasive pests. Various aspects of the biology of *Wolbachia* are still widely unexplored, particular ly its biological interactions, spread and acquisition: this knowledge is an important prerequisite to properly characterize the evolution of this taxon. To further understand the biodiversity and the evolution of *Wolbachia* we compare the phylogenet ic signals of two independent data sets: a gene-rich phylogenomic (GENOME) and a taxon- rich multilocus sequence typing (MLST) alignment. Our MLST data set provides a topology consistent with previous MLST phylogenies, but in conflict with the GENOME data set for the position of wZoo and wCte, infecting respectively termite and cat flea. These incongruences have been explored using various approaches to estimate intragenic recombination, evaluating strain misassignment and multiple *Wolbachia* infections on the same host species, and performing topology comparison tests. Results indicate that these discrepancies are due, at least partially, to undetected co-infectio ns, resulting in different *Wolbachia* strains being sampled in the GENOME and the MLST dataset. Coalescent aware phylogenies further show among genes incongruences for wZoo in the GENOME data set: this is compatible with either horizontal transfer, undetected co-infections, or poor gene sampling for certain *Wolbachia* strains. Overall, our results suggest that discrepancies between our MLST and GENOME dataset are not due to stochastic (poor signal in MLST) or systematic errors (signal misinterpretation), but are caused by the complex epidemiological pattern of *Wolbachia* which may have resulted in different strains being sampled in different specimens and/ or have resulted in chimeric genome assemblies.